

## Appendix A

### Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 2

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

to: SID 2 check: 1650 from: 1 to: 518

WPDEF SVBV E3 Promoter

Symbol comparison table: rwsgapdna.cmp CompCheck: 8760

Gap Weight: 50 Average Match: 10.000  
Length Weight: 3 Average Mismatch: 0.000

Quality: 4760 Length: 518  
Ratio: 10.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):  
! = IDENTITY  
: = 5  
. = 1

SID 1 x SID 2 October 12, 2004 11:44 ..

```
1 .....aactatgctgatgacaagataattctaataagcaat 36
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
1 ggatcccccaagcttaactatgctgatgacaagataattctaataagcaat 50
37 tattcagaattaatcaaggagaagaaattaataactcttcagaatatga 86
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
51 tattcagaattaatcaaggagaagaaattaataactcttcagaatatga 100
87 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 136
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
101 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 150
137 aatggtgtctcgatgcacccagaaccacatcttcagcagatgtgaagca 186
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
151 aatggtgtctcgatgcacccagaaccacatcttcagcagatgtgaagca 200
187 gccagagtggccacaagacgcactcagaaaaggcatcttccggacac 236
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
201 gccagagtggccacaagacgcactcagaaaaggcatcttccggacac 250
237 agaaaaagacaaccacacagctcatcatccaacatgttagactgtcgttatgc 286
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||
251 agaaaaagacaaccacacagctcatcatccaacatgttagactgtcgttatgc 300
287 gtcggctgaagataagactgaccccaaggccagcactaaagaagaaataat 336
```

||||||||||||||||||||||||||||||||||||||||||||  
301 gtcggctgaagataagactgacccaggccagcactaaagaagaaataat 350  
337 gcaagtggtccatgtccacttttagcttaataattatgtttcattatta 386  
||||||||||||||||||||||||||||||||||||||||  
351 gcaagtggtccatgtccacttttagcttaataattatgtttcattatta 400  
387 ttctctgttttgcctctatataaaagagcttgcattttcatttgaaggc 436  
||||||||||||||||||||||||||||||||||||  
401 ttctctgttttgcctctatataaaagagcttgcattttcatttgaaggc 450  
437 agaggcgaacacacacacagaacccctgcattacaaacc..... 476  
||||||||||||||||||||||||||||  
451 agaggcgaacacacacacagaacccctgcattacaaaccggatcggct 500

### Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 3

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

to: SID 3 check: 303 from: 1 to: 651

WPDEF seSVBV promoter  
1-108 of SVBV replaced by 92-362 of SBVB

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight: 50 Average Match: 10.000  
Length Weight: 3 Average Mismatch: 0.000

Quality: 3971 Length: 654  
Ratio: 8.342 Gaps: 1  
Percent Similarity: 85.201 Percent Identity: 85.201

Match display thresholds for the alignment(s):

|- IDENTITY  
:= 5  
::: 1

1 ..... aactatgctgatgacaagataattct 27  
151 cagaaaaaagacaaccacagctcatcatccaaacatgttagactgtcgat 200  
28 ataagcaattatttcagaattaatcaaggagaaaagaattaactcttc 77  
201 cgtcggtgtaaagataaagactgaccccccaggccagcactaaagaagaaataa 250  
78 agaataatgaagccccgtttacaagtggccagctagctatcactgaaaaqa 127  
251 tgcagaatgggtcttagct...ccactttagcgcctagctatcactgaaaaaga 297  
128 cagcaagacaatggtgtctcgatgcaccagaaccacatcttgcagcaga 177  
298 cagcaagacaatggtgtctcgatgcaccagaaccacatcttgcagcaga 347  
178 tgtgaagcagccagagtggtccacaagacgcactcagaaaaggcatcttc 227  
348 tgtgaagcagccagagtggtccacaagacgcactcagaaaaggcatcttc 397  
228 taccgcacacagaaaaagacaaccacagctcatcatccaaacatgttagactg 277  
398 taccgcacacagaaaaagacaaccacagctcatcatccaaacatgttagactg 447

278 tcgttatgcgtcggtgaagataagactgaccccaaggccagcactaaaga 327  
||||||||||||||||||||||||||||||||||||||||||||||||  
448 tcgttatgcgtcggtgaagataagactgaccccaaggccagcactaaaga 497  
||||||||||||||||||||||||||||||||||||||||  
328 agaaaataatgcaagtggcctagctccacttttagctttataattatgtt 377  
||||||||||||||||||||||||||||||||||||||||  
498 agaaaataatgcaagtggcctagctccacttttagctttataattatgtt 547  
||||||||||||||||||||||||||||||||  
378 tcattattattctctgtttgtctcttatataaagagcttgcatttca 427  
||||||||||||||||||||||||||||||||||||  
548 tcattattattctctgtttgtctcttatataaagagcttgcatttca 597  
||||||||||||||||||||||||||||  
428 ttgttgaaggcagaggcgaacacacacacacagaacacctccctgcttacaaacc. 476  
||||||||||||||||||||||||||||||||  
598 ttgttgaaggcagaggcgaacacacacacacacagaacacctccctgcttacaaaccg 647  
||||||||||||||||||||||||

Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 4

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVRV E3 Promoter fragment

to: SID 4 check: 7979 from: 1 to: 701

WPDEF leSVBV  
1-108 of SVBV replaced by 92-404 of SVBV

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight: 50 Average Match: 10.000  
Length Weight: 3 Average Mismatch: 0.000

Quality: 4049 Length: 704  
Ratio: 8.506 Caps: 2.  
Percent Similarity: 88.161 Percent Identity: 88.161

PERIODIC CHANGES IN THE ECOLOGY OF THE BROWN SPOTTED COWFISH, *I. punctatus*, IN THE GULF OF MEXICO

Match display thresholds for the alignment(s):  
| - IDENTITY  
: = 5  
. - 1

SID 1 x SID 4      October 12, 2004 11:46 ..

1 .....aactatgctgatgacaagataattctaataaaggcaattt 40  
201 gtcggctgaagataagactgaccccccaggccagcactaaagaagaataat 250  
41 cagaattaatcaaggagaa....agaattaataactcttcagaatatga 86  
251 gcaagtggtcttagctccactttagcttaataattatgtttcattatta 300  
87 agccccgtttacaagtggccagctagctatcactgaaaagacagcaagac 136  
301 ttctctgttt...ttgctctcgctagctatcactgaaaagacagcaagac 347  
137 aatggtgtctcgatgcaccagaaccacatcttgcagcagatgtgaagca 186  
348 aatggtgtctcgatgcaccagaaccacatcttgcagcagatgtgaagca 397  
187 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 236  
398 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 447  
237 agaaaaaaagacaaccacacagctcatcatccaaacatgttagactgtcgttatgc 286  
448 aaaaaaaaagacaaccacacagctcatcatccaaacatgttagactgtcgttatgc 497

287 gtcggctgaagataagactgaccccaggccagcactaaagaagaataat 336  
||||||||||||||||||||||||||||||||||||||||||||||||  
498 gtcggctgaagataagactgaccccaggccagcactaaagaagaataat 547  
||||||||||||||||||||||||||||||||||||||||||||  
337 gcaagtggtccctagctccactttagcttaataattatgtttcattatta 386  
||||||||||||||||||||||||||||||||||||||||||||  
548 gcaagtggtccctagctccactttagcttaataattatgtttcattatta 597  
||||||||||||||||||||||||||||||||||||||||  
387 ttctctgtttgtctctatataaagagcttgtatttcatttgaaggc 436  
||||||||||||||||||||||||||||||||||||||||  
598 ttctctgtttgtctctatataaagagcttgtatttcatttgaaggc 647  
||||||||||||||||||||||||||||||||||||  
437 agaggcgaacacacacacagaacccctgtttacaaacc..... 476  
||||||||||||||||||||||||||||||||||||  
648 agaggcgaacacacacacagaacccctgtttacaaaccggatcggt 697  
||||||||||||||||||||||||||||

## Multiple Sequence Alignment: SEQ ID NO: 1-4

Symbol comparison table: pileupdna.cmp CompCheck: 6876GapWeight: 5  
GapLengthWeight: 1SID\_1\_pileup\_405724.txt MSF: 716 Type: N October 8, 2004 12:10  
Check: 6538 ..

Name: SID_1	Len: 476	Check: 2120	Weight: 1.00
Name: SID_2	Len: 518	Check: 8412	Weight: 1.00
Name: SID_3	Len: 651	Check: 1160	Weight: 1.00
Name: SID_4	Len: 701	Check: 4846	Weight: 1.00

//

1	50
SID_1 ~~~~~	~~~~~
SID_2 ~~~~~	~~~~~
SID_3 ggatccgctt	tacaagtggc
SID_4 ~gatccgctt	tacaagtggc
	cacctagcta
	tcactgaaaa
	gacagcaaga
51	100
SID_1 ~~~~~	~~~~~
SID_2 ~~~~~	~~~~~
SID_3 caatgggtgc	tcgatgcacc
SID_4 caatgggtgc	tcgatgcacc
	agaaccacat
	cttgcagca
	qatgtgaagc
101	150
SID_1 ~~~~~	~~~~~
SID_2 ~~~~~	~~~~~
SID_3 agccagagtg	gtccacaaga
SID_4 agccagagtg	gtccacaaga
	cgcactcaga
	aaaggcatct
	tctaccgaca
151	200
SID_1 ~~~~~	~~~~~
SID_2 ~~~~~	~~~~~
SID_3 cagaaaaaga	caaccacagc
SID_4 cagaaaaaga	caaccacagc
	tcatcatcca
	acatgttagac
	tgtcggtatg
201	250
SID_1 ~~~~~	~aactatgt
SID_2 tcccccaagct	taactatgt
SID_3 cgtcggtcgtga	agataagact
SID_4 cgtcggtcgtga	agataagact
	gtgacaaga
	taatttctaat
	aagcaattat
	gtgacaaga
	taatttataat
	aagcaattat
	gaccccaaggc
	cgcactaaa
	gaagaaataaa
251	300
SID_1 tcagaattaa	tcaaggagaa
SID_2 tcagaattaa	tcaaggagaa
SID_3 tgcaagtgggt	cctagctcca
SID_4 tgcaagtgggt	cctagctcca
	agaattaata
	actcttcag
	aatatgaagc
	agaattaata
	actcttcag
	aatatgaagc
	ctttag....
	.....
	tttcattatt

301	350	
SID_1	ccgcttaca agtg.gccag	ctagctatca ctgtaaaagac agcaagacaa
SID_2	ccgcttaca agtg.gccag	ctagctatca ctgtaaaagac agcaagacaa
SID_3	..... .... cg	ctagctatca ctgtaaaagac agcaagacaa
SID_4	attctctgct tttgtctcg	ctagctatca ctgtaaaagac agcaagacaa
351		
SID_1	tggtgtctcg atgcaccaga	accacatctt tgcaaggat gtgaaggcgc
SID_2	tggtgtctcg atgcaccaga	accacatctt tgcaaggat gtgaaggcgc
SID_3	tggtgtctcg atgcaccaga	accacatctt tgcaaggat gtgaaggcgc
SID_4	tggtgtctcg atgcaccaga	accacatctt tgcaaggat gtgaaggcgc
401		
SID_1	cagagtggc cacaagacgc	actcagaaaa ggcatcttct acggacacag
SID_2	cagagtggc cacaagacgc	actcagaaaa ggcatcttct acggacacag
SID_3	cagagtggc cacaagacgc	actcagaaaa ggcatcttct acggacacag
SID_4	cagagtggc cacaagacgc	actcagaaaa ggcatcttct acggacacag
451		
SID_1	aaaaagacaa ccacagctca	tcatccaaaa tgtagactgt cgttatggt
SID_2	aaaaagacaa ccacagctca	tcatccaaaa tgtagactgt cgttatggt
SID_3	aaaaagacaa ccacagctca	tcatccaaaa tgtagactgt cgttatggt
SID_4	aaaaagacaa ccacagctca	tcatccaaaa tgtagactgt cgttatggt
501		
SID_1	cggctgaaga taagaatgac	ccaggccag cactaaagaa gaaataatgc
SID_2	cggctgaaga taagaatgac	ccaggccag cactaaagaa gaaataatgc
SID_3	cggctgaaga taagaatgac	ccaggccag cactaaagaa gaaataatgc
SID_4	cggctgaaga taagaatgac	ccaggccag cactaaagaa gaaataatgc
551		
SID_1	aagtggctc agtccactt	tagttttat aattatgttt cattattatt
SID_2	aagtggctc agtccactt	tagttttat aattatgttt cattattatt
SID_3	aagtggctc agtccactt	tagttttat aattatgttt cattattatt
SID_4	aagtggctc agtccactt	tagttttat aattatgttt cattattatt
601		
SID_1	ctctgtttt gctctctata	taaagagctt gtatttcat ttgaaggcag
SID_2	ctctgtttt gctctctata	taaagagctt gtatttcat ttgaaggcag
SID_3	ctctgtttt gctctctata	taaagagctt gtatttcat ttgaaggcag
SID_4	ctctgtttt gctctctata	taaagagctt gtatttcat ttgaaggcag
651		
SID_1	aggcgaacac acacacagaa	cctccctgtt taaaacc~~ ~~~~~
SID_2	aggcgaacac acacacagaa	cctccctgtt taaaaccgg atcgggctgc
SID_3	aggcgaacac acacacagaa	cctccctgtt taaaaccgg atc~~~~~
SID_4	aggcgaacac acacacagaa	cctccctgtt taaaaccgg atcgggctgc
701		
SID_1	~~~~~ ~~~~	716
SID_2	aggctctctaa ccatgg	
SID_3	~~~~~ ~~~~	
SID_4	ag~~~~~ ~~~~	